

Figure 1 A.

BD fusion	AD fusion	-His growth	-Leu growth	$\beta$ -gal activity	-Ade-Trp growth
MPK4	MKS1	+	+	+	+
MKS1	MPK4	+	+	+	+
MKS1	MPK3	-	-	-	+
MKS1	MPK5	-	-	-	+
MKS1	MPK6	-	-	-	+
MKS1	MPK17	-	-	-	+
MKS1	WRKY25	+	+	+	+
MKS1	WRKY33	+	+	+	+
MKS1	WRKY26	-	-	-	+
MKS1	WRKY29	-	-	-	+
MPK4	WRKY25	-	-	-	+
MPK4	WRKY33	-	-	-	+

Figure 1B (1)

1-----Pep22-----1

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1 MSSTSSSPPPPSK-----AKRRCGLHGARPOLIVSSAPAEASRPSKKPRVS-----GGG
1 MSSTSSSPPPPSK-----AKRRCGLHGARPOLIVSSAPAEASRPSKKPRVS-----GGG
1 MTMTVATMPSSDASSSPPKRPTATGGGILGPRRPELKVTS SSPSSSSSSSRSSSPAS-NKP-----PASTT
1 MTMTVAMPSSS-----SSRGGDLRGPRPELKVSSSSSRGSSPSSSASKG-----ASKK
1 -----SLOGPRPEPLILPPGSGTTSSSSSSSTPRPA-KRPRRVVSGGGGDVSRAPQSSA
1 -----MDPSEYFAGGNPSDQONQKRLQICGPRPELKVSHKDSHKIKKPP-----KHPAPPP-NRDQPPPY
1 -----MDPSESFAGGNPSDQONQKRLQICGPRPELKVSHKDSHKIKKPP-----KHPAPPPQ-HRDQAPLY
1 -----MDPSEHFAGGNPFDQQTPEKRLQICGPRPELKVSHKDSHKIKKPP-----RHPAPPPQHHRDQAPLY
1 -----SLOGPRPEPLRINKDSHKIKKPP-----LAPQPSHP-----HQP
1 -----MDNRSPSRGILGPRPELKVGRDSHKIKKPPPLAPP-----PQPQPPQTHQOEPSQSR
1 MEFPSSSTSPSPSSGQHQQOPTTFRROLOGPRPELNVRMESHAKKPSGAAAA--AAQAQAHQLPAQAQARREQQOP
1 MDPPSSSG-----RPTTFRROLOGPRPELNVRMESHAKKPS-----ASGAPPAPGQGRPRDHHHHHPQ
1 -----QGRPEPLAVSKDSHKYRKPFVAPQROQHQQQPAQQLQQQOQHQQOQQO
1 -----MDQSSSTLLINQ-----RKSSSSPTTRIPPKOK-----RKSTT
1 -----MESSSSTFLTTSILDKKPSPVSRKSPKOK-----KKTTS
1 -----MVRNSMKAEDIDHLPHTFYGDYSKTLVPMNNS-----QIITK
1 -----MEITQYQSFH-EGSSSRVSMNNS-----QVISK
1 -----MEATIFEKRESSLSIAVHKOS-----YSITK
1 -----MEIEATTVOKRRS-LPTIAVHKOS-----RTLTK
1 -----MEQQLSSPSASQSGGRELQGRPEPLKVRSKSHKIKKOE-----PVQ
1 -----MIPTRCNEINGSRPSLSKLAGESSHATIKTSCKSKP-----RPH
1 -----MPSRSSMASPLLRPHDLLGPRPEPLKVSTGTTTGTADLQLOVVN-----RR
1 -----MDROQQSSRGNATATRGGGSSGSGGGGGVG-----KAA
1 -----MAAASFDAADVTRRGGTGRAIGVHAASHKIKKPPGAG-----HGQ
1 -----MSKAAKN-----
1 -----NFKDVIQRLTKPEDNKQPAKAGEVSPAER-----LASI
r i gpr l v dsh ikk tk
DOMAIN 1

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1C3 DELETION

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51 GDTGPVIVYEL-PRVHVHVEQEEFMVVKLTGG-----KQOPAAASTLTTL
51 GDTGPVIVYELTPRVHVHVEQEEFMVVKLTGG-----KQOPAAASTLTTL
56 AKRPPVIVYEHTPRVVIHASPOEFMTVVRLTG-----KRPRAAPTSS--
50 SAAAPVIVYEHTPKVVIHARPOEFMTVVRLTG-----KPPAAPVVMMPA
53 AAPGPVIVYEHTPKVVIHARADEPKALVQSLTG-----RGGCEAVER--
61 IPREPVIIVYAVSPKVVHATASEFMNVVORLTGISSGV-----FLESGGGDVSPAAR
62 AAREPVIIVYAVSPKVVHTIASDFMNVVORLTGISSAV-----FLESNGGDVSPAAR
63 PPREPVIIVYAVSPKVVHTTISDFMNVVORLTGISSEV-----FLESNDGDVSPAAR
35 PPROPIIIVYTVSPKVIHTTTPSDFMNLVORLTGSSSSS-----SAEVVMSNNNN--
56 PPPGPVIIIVYTVSPRIIHTHPNNFTLVORLTGKTSTS-----TTSSSYSSSTSA PKD
79 PPRAPVIIYDASPKVIHAKPNEFMALVORLTGPGSGPPAPPHQGEAQADYPMDEAAAAQFFPELLLSPSAMSPAAR
61 PGRAPVIIYDASPKVIHAKPSEFMALVORLTGPGAQAQHERHVADDDATAN--GGGVLGQAFLPELLLSPSAMSPAAR
52 QGRAPVIIYDASPKVIHTKPGDFMALVORLTGPGSTSQAQFDAAAAAAGPS----HPAAMEFEPREFLLSPTAALSPAAR
33 THKPIKIRVYISNPMRVETCPSEKRELVQELTG-----QDAVDLQEEPI
36 TNKPIKIRVYISNPMRVQTCASEKRELVQELTG-----QDAVDLQEEPI
41 IKPKIRIHHIFAPEELIKTDVKNERTLVQSLTG-----KPE--LTKTGS
29 IKPKIRIHHIFAPEELIKTDVKNERSLVQSLTG-----KPAPGEAKTGK
28 SKPKIRIHHIFAPEELIKTDVANERELVQSLTG-----KPDQRTSKAK
29 SKPKIRIHHIFAPEELIKTDVANERETVQNLTG-----KQDHHHEDLPH
44 QLRPVPVIIYVSPKVVHANADFMNVVORLTG-----APPTAPPQEPH
40 GRASEPVIIVYAHSPKVIHTRAEDFMALVORLTG-----LDEIIRNFSSESS
50 RRRPVPVIIYVESPVVHAHPERKSVVORLTG-----TAPALELEPL
35 GGRPIKIVYISNPMRVKTSAAGERALVQELTG-----ENADPSKYSRP
43 QRRPVPVIIYVSPKVIHVDAAHEFMVORLTG-----PEAGRGDRKSRPS
8 -MTVPKIRIVINTQILETDASSERSVORLTG-----NSTVEMVAAAPP
35 QRTSPKKKQRFVNRDEHMMQMLDEGVQMGQVPG-----ILLSSTLPP
kr pviiv SPkviht efm lVQrLTG rpaeevSP pr
DOMAIN 2

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Figure 1B (2)

!C2 DELETION

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96 PAADQVAGGDHAAAAAADPTVLTG--QORQAPAPAPALDGDHPAAPPSPADA-----FILSPSSFFLSPTTMBALQ
97 PAADQVAGGDHAAAAAADPTVLTLGQORQAPAPAPALDGDHPAAPPSPADA-----FILSPSSFFLSPTTMBALQ
108 --LPSGTVSPAATAEAGGCDPILLITLGGORQ--AAAPAPPTTILLPSSAMAAAG-----MLSPG--FIESPSTMOAIQ
94 YDAPAMVEQCAAAACAGGDPILLITLGGORQ--AASAPAPPPAVPSP--MAAG-----MLSPG--FIESPSTMOAIQ
95 -----PPASSQOTACOLLVLTLGHHQH--VPPPPP--LPSP--GCAAG-----FILSPGSEFESPATMOAIQ
113 LAATENASPRGCKE-----PAARDETVEINTAMEEAEFFGGYAPGILSPSPAI-----LPTASTGTFSPMYHOCGM
114 LAATENASPRGCKEPV-----MAAKDETVEITAMEEAEFFSGYAPGILSPSPAM-----LPTASAGTFSPMYHOCGM
115 LAATENASPRGCKE-----PVESSTAMEEAEFFGCVYPGILSPSPAM-----LPTVPAGTFSPMFHLCGL
83 -----TTHVDFENNGCGGVSPAPARYATHEKAM-----SPMCKKENVLLSVNNIIS
108 ASTMVDTSGLISPAARFVTEKANTSNELCTFVGGEETMDQYYHYHHHHHHQH-----QOHONOCFERPSFHHAGT
159 LATIERSVRPMP-----EPABEYVDITNGGCGCGVDDCGTAAILGSIIRPGILSP--LPSSLPPAAVPCQESPLPFDASC
139 LATIERSVRPVP-----APAPAPDYAADG-----HPRGGARPREAPR--HPVPAAVLAAAGRRVGPVIAAAL
128 LATIERSVRPLPPHAPAAVEPYFGATNDDCFELPGSADMDSLAALGPPACRPGILSPAALPPAASTGLFSPMPFDSC
76 TF-----TAVDLHRPCESENNLEP-----LDGEVRCEYYSPDEEVFNAP--QM-----SAGLSGTFSSG
79 YS-----PSSDDHNLSPPAENLAPRVLHQPFFGERDSDCYEPLNAEDMFLPDQM-----SAGFSGTFSSNG
82 KK-----KITNTNFPAPPCLQODSGQEHAEIDNRIG--SHYVKEEWGS-----SSNTNTYEDFDGLIDLD
72 KR-----AKSRITPQEPVCDHQPVRNLSGFTGLLANGGNHGVKEEWGSGDQS-----TSNTNTYEDLEGLIQDV
71 PR--RDMERLHRQVQDMINTEKLREPEHCDQEFCLNAEETSMTWNGNNGAGESS-----GGFLNCTGDFEGFIQEL
72 QKGLKRNPSRRSHDHHEVDMNKSNGFCINSDEEEECMVSMTWNGN--GDESS-----GGFLNCTGDLGDFIQEL
88 HPTLLAQMPQPSPFPFHLQQODAWPQQCHSPAALQAAARSSCADLPLPLSILSP--VPGTVLPAIPASEFSPSPSILSPV
85 SSVVTEEVNVGDDNTAAPPFSDRTORQKLTDMPLFTPSSTMLFSGPTQLMYMSF-----NRDTSERPLVFKSE-
91 KFFHFHFHFPSSVGAASRALLETSSSTSSGVMSVVTVDITCGGCGSPVQOENHH-----MLVSSDPCDLPPLPSILSPV
78 ASADDDDDGGCGGGGGGELAAASDGAGEFGPQAAASPDTGAAASDAADALVAAG-----HPAAATEDDEGGGGGG
88 TSGVGGGAGEAPSEGAENKTRAPPVRVKARALNRPVSVTTRRQQAADASP-----PSGLMLFQDLSPERGA
53 PTAAANYVREGYNWDDQSSRALISETESIARKPSPLGRGMSFNDFDNTEKELP-----RVDDLRLLYADEYRSNY
80 ISSENFSLSLSPSTPLYTFSPETFSPTSYIFSPEKNMLVPSNIDRKGTIPTMQS-----EVYPMNMHQRILSKFLGG
aam h aat a aa pl tltq a am aa lt la g m aal lpsa sgifSP tm a m

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!C1 DELETION

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168 EEEAARRVVEATSTGLGVQSGKSSQDTVNLHADANAAAAAALAAHSSRGPRSSSTOPP-----a
170 ELAALF-----b
177 ELNPLF-----c
162 ELSPLF-----d
152 EIIS-----e
179 FS-----PAIPLGLFSPAGFMSFPRSPGFT-----SLVASPTFADFFSHIWDQD-----f
182 MF-----SPG--LFSPAGLMSFPG--FA-----SLVASPTFADLFSHIWG-----g
175 FS-----PALPPGLFSPAGLMSPGYAS-----LASPNFADFFSHIWDP-----h
129 DV-----E-----i
180 LSPGPNLSLPSVSPDFSTIGPTDPQGFSSFFNDFNSILQSSPSKIQSPSSMDLFNNFFDS-----j
231 ISWLNELSPIIRAASAGAASSSGGGGSGCNTSNGGAARPPPSYYADPFVPSPRHLLATPTVPSPATCAELFSNLPDLk
199 RPQORQLAQRAQPHPPGVSVEGQRSAPLAHAGPTGGSROP-----l
208 LSWLSELSPFLPSAGTRAAAGLLDQAPFAPSRSRSLLLSTPTMPS--PATFSVLEFFSSPNFPDL-----m
129 -----FYNVNALGSIGSL-----n
139 -----FYNVNDFGSIDSM-----o
142 -----EDDNIFSSRWFDLQQQ-----p
138 GEDYFSSFFMRSSSSSQVEGFIFNNNNNNNNNNNNNNNNNNNTNFDTKAHNSS-----q
140 G-----EFPYLPLSSIDASASSNSSS-----r
141 G-----EFPYLFTTIDPAVASSSHLGNVFAEPHHA-----s
166 PFLGATTTSSAAPSTSPSPMGGSAYYWDLFNMQQQQHYHHQ-----t
-----u
165 SSNTTAVVSSSTNTSKNYE-----v
148 GYDDDDDDIFRSQLLDTYSVFSPTLLYDHPHSHV-----w
159 LKGEHLPLVSPAHLHVGDFHFLSPAGAAAALGSPSPSEVDDIFGTLSSQQQ-----x
125 -----y
156 AKPP-----z

```

a: OsBAC15955	b: Os8355.t00567	c: ZmCC661221	d: Os8360.t05160	e: ZmBM340911
f: MKS1 At3g18690	f: BoBH544707	g: BoBOHBT92TR + BOGQI24TF	h: GmBE020960	
i: At1g21326	j: OsCAD40925	k: ZmCC613160	l: ZmCC635639	m: At2g41180
n: AtAL390921	o: AtAL138658	p: At2g44340	q: AtT46022	r: At2g42140
s: OsAP004654	t: At1g68450	u: ZmCC442903	v: OsAP003260	w: ZmCC700850
x: Ntacre169	z: MtAC143340.1			

Figure 2.

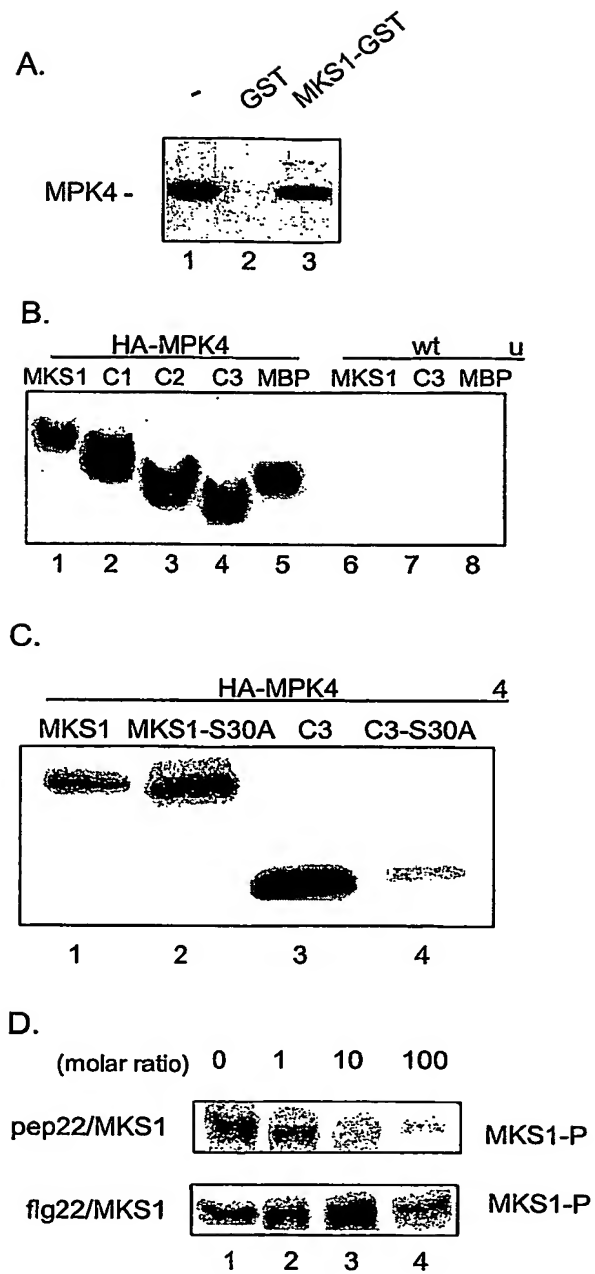


Figure 3.

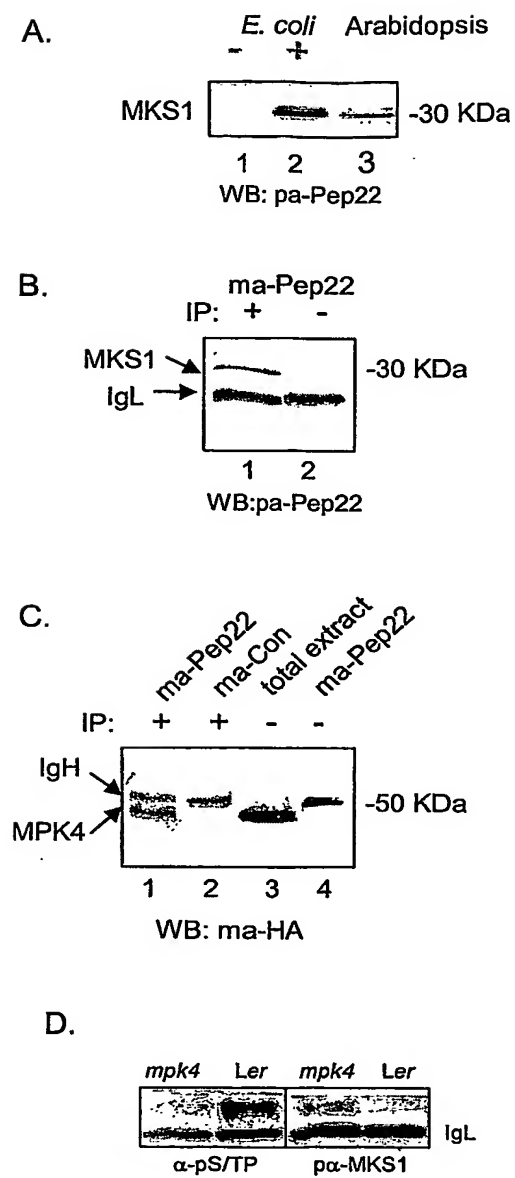
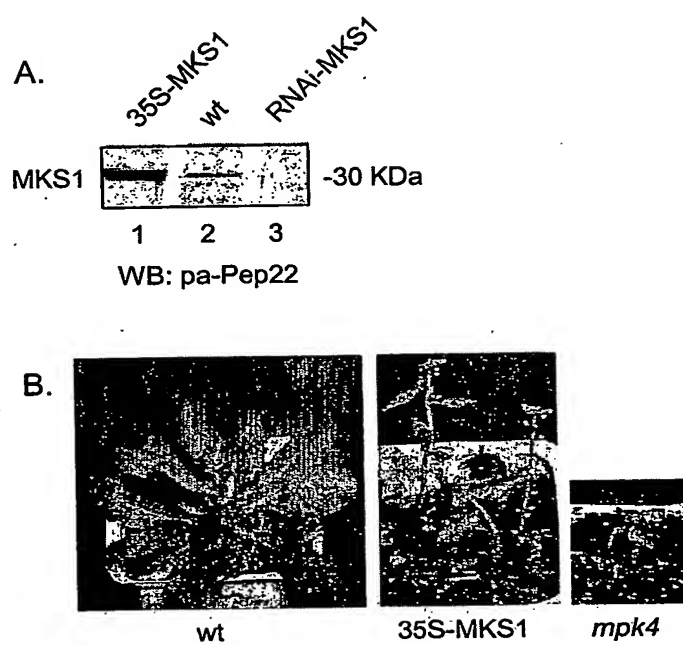
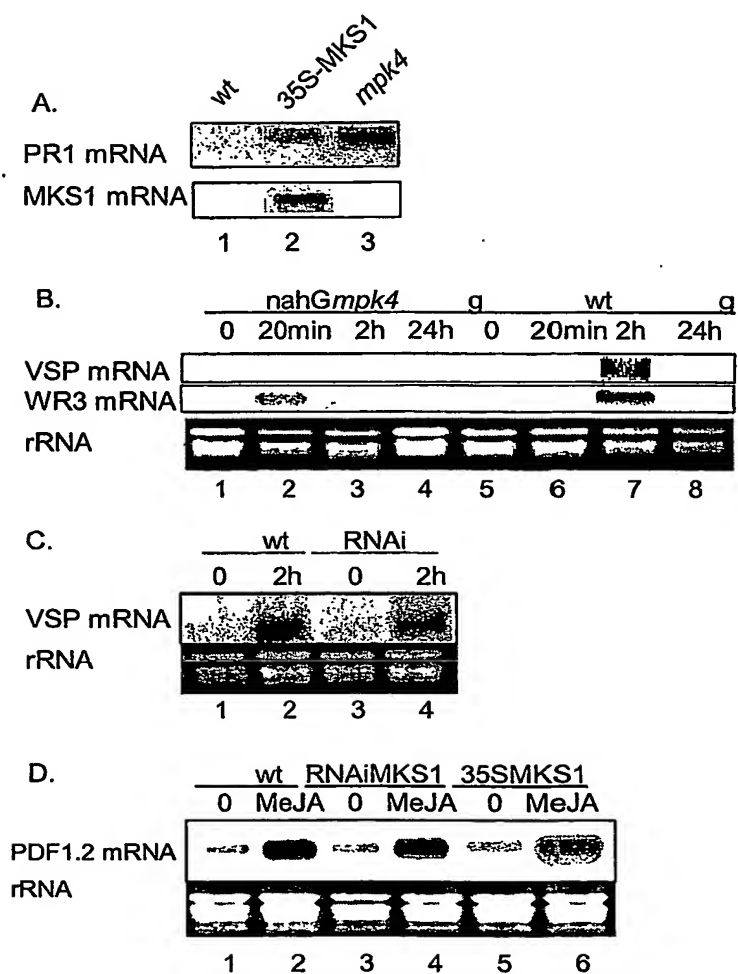


Figure 4.



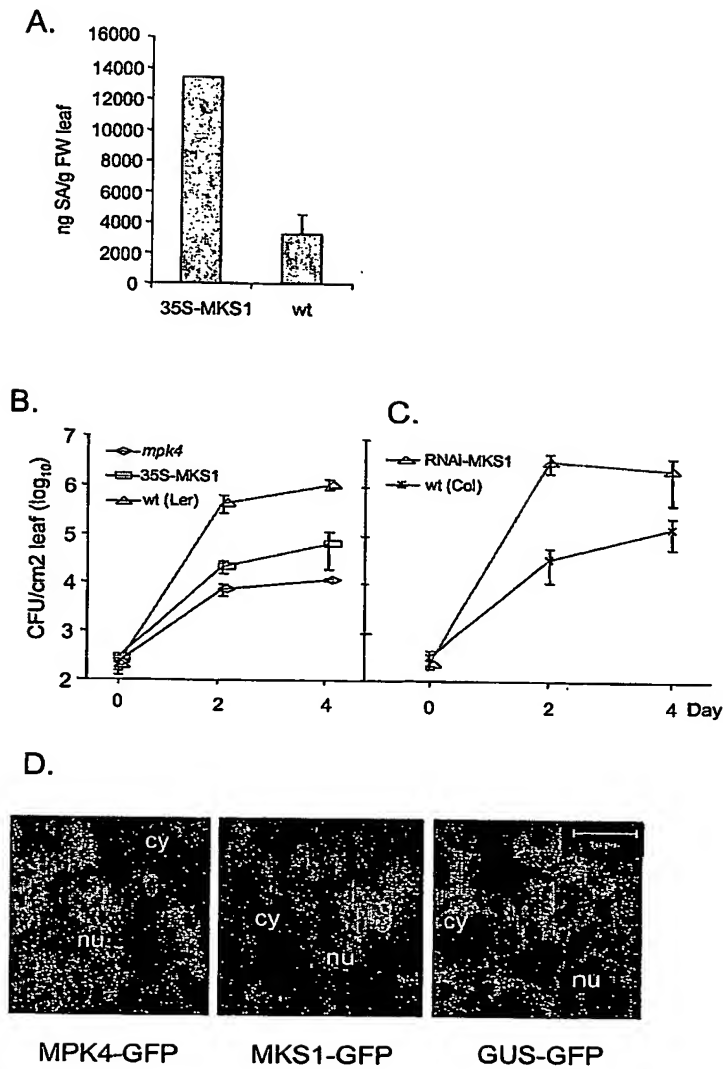
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Figure 5.



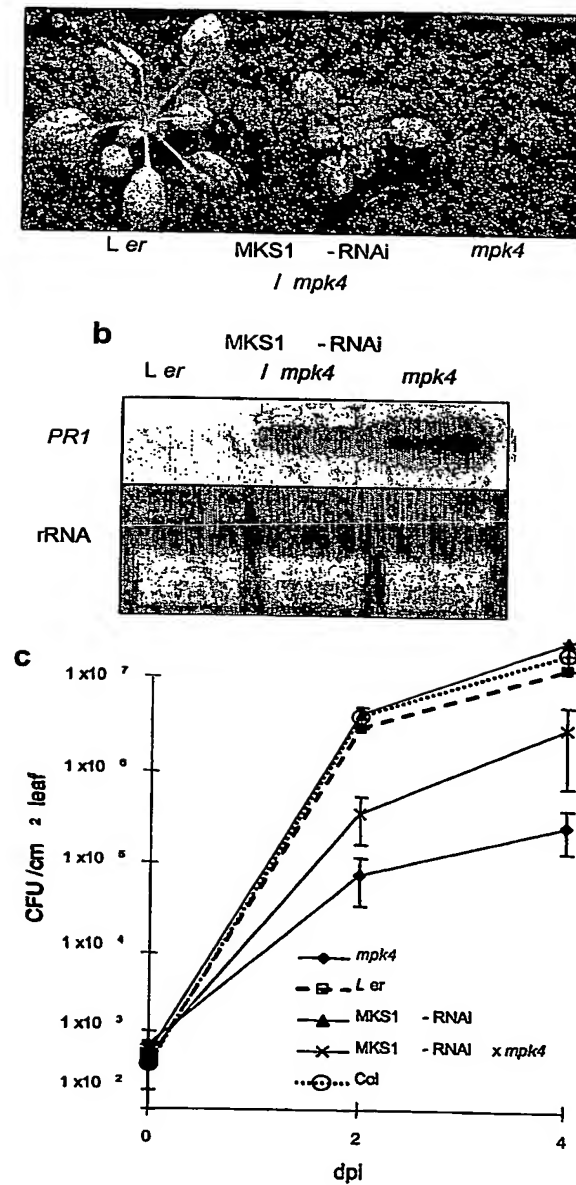
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Figure 6.



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Figure 7



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Figure 8.

